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calling said unknown base according to results of said comparing step [said comparison of said plurality of probe intensities].

B2  
3. (Amended) The method of claim 1 [2], wherein said comparing step includes [further comprising] the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

4. (Amended) The method of claim 3, wherein said calling step includes [further comprising] the step of calling said unknown base as being a base according to [complement of] said probe associated with said higher probe intensity if said ratio is greater than a predetermined ratio value.

B3  
6. (Amended) The method of claim 1 [2], further comprising the step of sorting said plurality of probe intensities.

B4  
8. (Amended) The method of claim 7, wherein said comparing step includes [further comprising] the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to probe intensities hybridizing with said reference sequence.

9. (Amended) The method of claim 7, wherein said comparing step includes [further comprising] the step of calculating first ratios of a wild-type probe intensity to each probe intensity of a probe hybridizing with said reference sequence, wherein said wild-type probe intensity is associated with a wild-type probe.

10. (Amended) The method of claim 9, wherein said comparing step includes [further comprising] the step of calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

B4  
11. (Amended) The method of claim 10, wherein said comparing step includes [further comprising] the step of calculating third ratios of said first ratios to said second ratios.

12. (Amended) The method of claim 46 [7], wherein said comparing step includes [further comprising] the step of comparing said ratio of neighboring nucleic acid probes [neighboring probe intensities of said plurality of probe intensities].

B5  
14. (Amended) The method of claim 13, wherein said comparing step includes [further comprising] the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to statistics about said plurality of experiments.

Please add claims 45-59 as follows.

B6  
1 -- 45. The method of claim 11, wherein said calling step  
2 includes the step of calling said unknown base according to said  
3 probe associated with a highest third ratio.

1 46. The method of claim 7, wherein said comparing step  
2 includes the step of calculating a ratio of a highest probe  
3 intensity of a probe hybridizing with said reference sequence to  
4 a highest intensity of a probe hybridizing with said sample  
5 sequence.

1 47. In a computer system, a method of identifying an  
2 unknown base in a sample nucleic acid sequence, said method  
3 comprising the steps of:

4 inputting a plurality of probe intensities, each of  
5 said probe intensities being associated with a nucleic acid  
6 probe;

7 said computer system comparing said plurality of probe  
8 intensities wherein each of said plurality of probe intensities

9 is substantially proportional to said associated nucleic acid  
10 probe hybridizing with said sample sequence; and  
11 calling said unknown base according to results of said  
12 comparing step.

1 48. The method of claim 47, wherein said comparing  
2 step includes the step of said computer system calculating a  
3 ratio of a higher probe intensity to a lower probe intensity.

Be 1 49. The method of claim 48, wherein said calling step  
2 includes the step of calling said unknown base according to said  
3 probe associated with said higher probe intensity if said ratio  
4 is greater than a predetermined ratio value.

1 50. The method of claim 49, wherein said predetermined  
2 ratio value is approximately 1.2.

1 51. In a computer system, a method of identifying an  
2 unknown base in a sample nucleic acid sequence, said method  
3 comprising the steps of:

4 inputting a first set of probe intensities, each of  
5 said probe intensities in said first set being associated with a  
6 nucleic acid probe and substantially proportional to said  
7 associated nucleic acid probe hybridizing with a reference  
8 nucleic acid sequence;

9 inputting a second set of probe intensities, each of  
10 said probe intensities in said second set being associated with a  
11 nucleic acid probe and substantially proportional to said  
12 associated nucleic acid probe hybridizing with said sample  
13 sequence;

14 said computer system comparing at least one of said  
15 probe intensities in said first set and at least one of said  
16 probe intensities in said second set; and

17 calling said unknown base according to results of said  
18 comparing step.

1           52. The method of claim 51, wherein said comparing  
2 step includes the steps of:

3           calculating first ratios of a wild-type probe intensity  
4 to each probe intensity of a probe hybridizing with said  
5 reference sequence, wherein said wild-type probe intensity is  
6 associated with a wild-type probe; and

7           calculating second ratios of the highest probe  
8 intensity of a probe hybridizing with said sample sequence to  
9 each probe intensity of a probe hybridizing with said sample  
10 sequence.

Be 1           53. The method of claim 52, wherein said comparing  
2 step further includes the step of calculating third ratios of  
3 said first ratios to said second ratios.

1           54. The method of claim 53, wherein said calling step  
2 includes the step of calling said unknown base according to said  
3 probe associated with a highest third ratio.

1           55. The method of claim 51, wherein said comparing  
2 step includes the step of calculating a ratio of a highest probe  
3 intensity in said first set to a highest intensity in said second  
4 set.

1           56. The method of claim 55, wherein said comparing  
2 step further includes the step of comparing said ratio of  
3 neighboring nucleic acid probes.

1           57. In a computer system, a method of identifying an  
2 unknown base in a sample nucleic acid sequence, said method  
3 comprising the steps of:

4           inputting statistics about a plurality of experiments,  
5 each of said experiments producing probe intensities each being  
6 associated with a nucleic acid probe and substantially  
7 proportional to said associated nucleic acid probe hybridizing  
8 with a reference nucleic acid sequence;